

GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run On: March 3, 2003, 19:03:02 ; Search time 32017 seconds  
(without alignments)  
3515.934 Million cell updates/sec

Title: US-10-049-743-1  
Perfect score: 3868  
Sequence: 1 gaattcgacagcgccg.....ggcttggtgacgagaattc 3868

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 630880

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*

- 1: gb\_ba:\*
- 2: gb\_htg:\*
- 3: gb\_in:\*
- 4: gb\_om:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_sts:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vi:\*
- 15: em\_ba:\*
- 16: em\_fun:\*
- 17: em\_hum:\*
- 18: em\_in:\*
- 19: em\_mu:\*
- 20: em\_om:\*
- 21: em\_or:\*
- 22: em\_ov:\*
- 23: em\_pat:\*
- 24: em\_ph:\*
- 25: em\_pl:\*
- 26: em\_ro:\*
- 27: em\_sts:\*
- 28: em\_un:\*
- 29: em\_vi:\*
- 30: em\_htg\_hum:\*
- 31: em\_htg\_inv:\*
- 32: em\_htg\_other:\*
- 33: em\_htg\_mus:\*
- 34: em\_htg\_pln:\*
- 35: em\_htg\_rpd:\*
- 36: em\_htg\_mam:\*
- 37: em\_htg\_vrt:\*
- 38: em\_sy:\*
- 39: em\_htgo\_hum:\*
- 40: em\_htgo\_mus:\*
- 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	26	0.7	26	6	AR028693 Sequence
C 2	26	0.7	26	6	AR086504 Sequence
C 3	25	0.6	25	6	AR028694 Sequence
C 4	25	0.6	25	6	AR086505 Sequence
C 5	23	0.6	23	6	AR028695 Sequence
C 6	23	0.6	23	6	AR028696 Sequence
C 7	23	0.6	23	6	AR086506 Sequence
C 8	23	0.6	23	6	AR086507 Sequence
C 9	22	0.6	22	6	AR028698 Sequence
C 10	22	0.6	22	6	AR086509 Sequence
C 11	21	0.5	21	6	AR028691 Sequence
C 12	21	0.5	21	6	AR028692 Sequence
C 13	21	0.5	21	6	AR028699 Sequence
C 14	21	0.5	21	6	AR086502 Sequence
C 15	21	0.5	21	6	AR086503 Sequence
C 16	21	0.5	21	6	AR086510 Sequence
C 17	20	0.5	20	12	AB068351 Synthetic
C 18	20	0.5	30	6	AB6836 Sequence 20
C 19	19.8	0.5	24	6	A75929 Sequence 29
C 20	18.4	0.5	30	6	AB6832 Sequence 16
C 21	18.2	0.5	30	6	AR117872 Sequence
C 22	18	0.5	18	6	AR028700 Sequence
C 23	18	0.5	18	6	AR086511 Sequence
C 24	18	0.5	19	6	AR179243 Sequence
C 25	18	0.5	27	6	AR143939 Sequence
C 26	18	0.5	30	6	AX057066 Sequence
C 27	17.8	0.5	30	6	AX037190 Sequence
C 28	17.8	0.5	30	6	AX481912 Sequence
C 29	17.6	0.5	24	6	AX010291 Sequence
C 30	17.6	0.5	25	6	A27144 synthetic 1
C 31	17.4	0.4	28	6	AX040166 Sequence
C 32	17.4	0.4	28	6	AX356226 Sequence
C 33	17.4	0.4	29	6	E10625 PCR primer
C 34	17.4	0.4	29	6	E12084 PCR primer
C 35	17.4	0.4	30	6	AR099335 Sequence
C 36	17.4	0.4	30	6	AX037174 Sequence
C 37	17.4	0.4	30	6	AX105343 Sequence
C 38	17.4	0.4	30	6	E30024 Method for
C 39	17.4	0.4	30	6	E30025 Method for
C 40	17.4	0.4	30	6	I28718 Sequence 21
C 41	17.4	0.4	30	6	I89372 Sequence 21
C 42	17.2	0.4	24	6	AX443904 Sequence
C 43	17.2	0.4	25	6	AR144353 Sequence
C 44	17.2	0.4	25	6	AX447880 Sequence
C 45	17.2	0.4	26	6	AR089201 Sequence

ALIGNMENTS

RESULT 1  
AR028693/c  
LOCUS AR028693 26 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 9 from patent US 5858753.  
ACCESSION AR028693  
VERSION AR028693.1 GI:5940666  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.  
TITLE Lipid kinase  
JOURNAL Patent: US 5858753-A 9 12-JAN-1999;  
FEATURES Location/Qualifiers

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BASE COUNT 5 a 8 c 9 g 4 t
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1500 GGAACGCTGCTCTACATGTGGGCC 1525
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Db 26 GGAACGCTGCTCTACATGTGGGCC 1

RESULT 2
AR086504/c AR086504 26 bp DNA linear PAT 07-SEP-2000
LOCUS
DEFINITION Sequence 9 from patent US 5985589.
ACCESSION AR086504
VERSION AR086504.1 GI:10013270
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
TITLE Lipid kinase
JOURNAL Patent: US 5985589-A 9 16-NOV-1999;
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BASE COUNT 5 a 8 c 9 g 4 t
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 26 GGAACGCTGCTCTACATGTGGGCC 1

RESULT 3
AR028694/c AR028694 25 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 10 from patent US 5858753.
ACCESSION AR028694
VERSION AR028694.1 GI:5940667
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
TITLE Lipid kinase
JOURNAL Patent: US 5858753-A 10 12-JAN-1999;
FEATURES
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ORIGIN

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Db 25 GCGGACTGCCCATTCCTGGGCC 1

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AR086505/c AR086505 25 bp DNA linear PAT 07-SEP-2000
LOCUS
DEFINITION Sequence 10 from patent US 5985589.
ACCESSION AR086505
VERSION AR086505.1 GI:10013271
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
TITLE Lipid kinase
JOURNAL Patent: US 5985589-A 10 16-NOV-1999;
FEATURES
source
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BASE COUNT 4 a 9 c 10 g 2 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 25 GCGGACTGCCCATTCCTGGGCC 1

RESULT 5
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LOCUS
DEFINITION Sequence 11 from patent US 5858753.
ACCESSION AR028695
VERSION AR028695.1 GI:5940668
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
TITLE Lipid kinase
JOURNAL Patent: US 5858753-A 11 12-JAN-1999;
FEATURES
source
1. .23
/organism="unknown"
BASE COUNT 4 a 6 c 10 g 3 t
ORIGIN

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Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 CCCTGGAGCAGCCGTTCCGCATC 1171
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Db 23 CCCTGGAGCAGCCGTTCCGCATC 1

RESULT 6
AR028696/c AR028696 23 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 12 from patent US 5858753.
ACCESSION AR028696
VERSION AR028696.1 GI:5940669
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
TITLE Lipid kinase
JOURNAL Patent: US 5858753-A 12 12-JAN-1999;
FEATURES
source
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/organism="unknown"
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Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2557 CATGCTGACCCCTGCAGATGAT 2577
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Db 1 CATGCTGACCCCTGCAGATGAT 21

RESULT 12
AR028692/c
LOCUS      AR028692      21 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 8 from patent US 5858753.
ACCESSION  AR028692
VERSION     AR028692.1 GI:5940665
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 21)
AUTHORS     Chantray,D.H., Hoekstra,M.F. and Holtzman,D.A.
TITLE       Lipid kinase
JOURNAL     Patent: US 5858753-A 8 12-JAN-1999;
FEATURES    Location/Qualifiers
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             1..21
             /organism="unknown"

BASE COUNT      4 a      9 c      4 g      4 t
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Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2899 CCGAGAGAGTGGGCGAGCTGTT 2919
|||||
Db 21 CCGAGAGAGTGGGCGAGCTGTT 1

RESULT 13
AR028699/c
LOCUS      AR028699      21 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 16 from patent US 5858753.
ACCESSION  AR028699
VERSION     AR028699.1 GI:5940672
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 21)
AUTHORS     Chantray,D.H., Hoekstra,M.F. and Holtzman,D.A.
TITLE       Lipid kinase
JOURNAL     Patent: US 5858753-A 16 12-JAN-1999;
FEATURES    Location/Qualifiers
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             1..21
             /organism="unknown"

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Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2712 TCAACAAGAGCAACATGGCAG 2732
|||||
Db 21 TCAACAAGAGCAACATGGCAG 1

RESULT 14
AR086502
LOCUS
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DEFINITION      Sequence 7 from patent US 5985589.
ACCESSION       AR086502
VERSION         AR086502.1 GI:10013268
KEYWORDS        .
SOURCE          Unknown.
ORGANISM        Unclassified.
REFERENCE       1 (bases 1 to 21)
AUTHORS         Chantray,D.H., Hoekstra,M.F. and Holtzman,D.A.
TITLE           Lipid kinase
JOURNAL         Patent: US 5985589-A 7 16-NOV-1999;
FEATURES        Location/Qualifiers
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                 1..21
                 /organism="unknown"

BASE COUNT      5 a      6 c      5 g      5 t
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Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2557 CATGCTGACCCCTGCAGATGAT 2577
|||||
Db 1 CATGCTGACCCCTGCAGATGAT 21

RESULT 15
AR086503/c
LOCUS      AR086503      21 bp      DNA      linear      PAT 07-SEP-2000
DEFINITION Sequence 8 from patent US 5985589.
ACCESSION  AR086503
VERSION     AR086503.1 GI:10013269
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 21)
AUTHORS     Chantray,D.H., Hoekstra,M.F. and Holtzman,D.A.
TITLE       Lipid kinase
JOURNAL     Patent: US 5985589-A 8 16-NOV-1999;
FEATURES    Location/Qualifiers
             source
             1..21
             /organism="unknown"

BASE COUNT      4 a      9 c      4 g      4 t
ORIGIN

Query Match      0.5%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2899 CCGAGAGAGTGGGCGAGCTGTT 2919
|||||
Db 21 CCGAGAGAGTGGGCGAGCTGTT 1

Search completed: March 4, 2003, 05:06:16
Job time : 32020 secs
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GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2003, 19:00:52 ; Search time 739 Seconds  
(without alignments)  
11787.185 Million cell updates/sec

Title: US-10-049-743-1

Perfect score: 3868

Sequence: 1 gaattcgccagcagcgccg.....ggctctgggtacgagaattc 3868

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 1875172

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_101002.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	26	0.7	26	19 AAV31345	Phosphatidylinositol
C 2	26	0.7	26	20 AAX15937	PCR primer used to
C 3	26	0.7	25	21 AAZ32887	Human PI 3-kinase-
C 4	25	0.6	25	19 AAV31346	Phosphatidylinositol
C 5	25	0.6	25	20 AAX15938	PCR primer used to
C 6	25	0.6	25	21 AAZ32888	Human PI 3-kinase-
C 7	23	0.6	23	19 AAV31347	Phosphatidylinositol
C 8	23	0.6	23	19 AAV31348	Phosphatidylinositol
C 9	23	0.6	23	20 AAX15939	Probe used to isol

C 10	23	0.6	23	20 AAX15940	Probe used to isol
C 11	23	0.6	23	21 AAZ32889	Human PI 3-kinase-
C 12	23	0.6	23	21 AAZ32890	Human PI 3-kinase-
C 13	22	0.6	22	19 AAV31350	Phosphatidylinositol
C 14	22	0.6	22	20 AAX15942	PCR primer used to
C 15	22	0.6	22	21 AAZ32892	Human PI 3-kinase-
C 16	21.4	0.6	29	21 AAO3873	Polymorphic fragme
C 17	21	0.5	21	19 AAV31343	Phosphatidylinositol
C 18	21	0.5	21	19 AAV31344	Phosphatidylinositol
C 19	21	0.5	21	19 AAV31351	PCR primer used to
C 20	21	0.5	21	20 AAX15935	PCR primer used to
C 21	21	0.5	21	20 AAX15936	PCR primer used to
C 22	21	0.5	21	20 AAX15943	PCR primer for hum
C 23	21	0.5	21	21 AAX13156	Human PI 3-kinase-
C 24	21	0.5	21	21 AAZ32885	Human PI 3-kinase-
C 25	21	0.5	21	21 AAZ32886	Human PI 3-kinase-
C 26	21	0.5	21	21 AAZ32893	PI3K antisense inh
C 27	20	0.5	20	21 AAX13114	PI3K antisense inh
C 28	20	0.5	20	21 AAX13115	PI3K antisense inh
C 29	20	0.5	20	21 AAX13116	PI3K antisense inh
C 30	20	0.5	20	21 AAX13117	PI3K antisense inh
C 31	20	0.5	20	21 AAX13118	PI3K antisense inh
C 32	20	0.5	20	21 AAX13119	PI3K antisense inh
C 33	20	0.5	20	21 AAX13120	PI3K antisense inh
C 34	20	0.5	20	21 AAX13121	PI3K antisense inh
C 35	20	0.5	20	21 AAX13122	PI3K antisense inh
C 36	20	0.5	20	21 AAX13123	PI3K antisense inh
C 37	20	0.5	20	21 AAX13124	PI3K antisense inh
C 38	20	0.5	20	21 AAX13125	PI3K antisense inh
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C 42	20	0.5	20	21 AAX13129	PI3K antisense inh
C 43	20	0.5	20	21 AAX13130	PI3K antisense inh
C 44	20	0.5	20	21 AAX13131	PI3K antisense inh
C 45	20	0.5	20	21 AAX13132	PI3K antisense inh

#### ALIGNMENTS

RESULT 1  
AAV31345/C  
ID AAV31345 standard; DNA; 26 BP.  
XX  
AC AAV31345;  
XX  
DT 12-OCT-1998 (first entry)  
DE Phosphatidylinositol 3-kinase p110 delta subunit RACE primer.  
XX  
KW Phosphatidylinositol 3-kinase; p110 delta; human; immune system;  
KW carcinogenesis; diagnosis; PCR; primer; RACE; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9823760-A1.  
XX  
PD 04-JUN-1998.  
XX  
PF 25-NOV-1997; 97WO-US21655.  
XX  
PR 25-NOV-1996; 96US-0777405.  
XX  
PA (ICOS-) ICOS CORP.  
PI Chantry DH, Hoekstra MF, Holtzman DA;  
XX  
XX WPI; 1998-322736/28.  
XX  
XX New phosphatidylinositol 3-kinase catalytic subunit - used to  
PT develop products for modulating kinase activity in immune system

PT signalling and in carcinogenesis  
 PS Example 1; Page 11; 53pp; English.  
 XX

CC 2 Antisense gene-specific oligonucleotide primers (see AAV31345 and  
 CC AAV31346) respectively comprise a primary RACE primer and a nested  
 CC RACE primer, and are based on the 5' end of M#928, a cDNA clone  
 CC obtained from human macrophage cDNA by PCR amplification (see  
 CC AAV31343-44). They were used to amplify 5' sequences of human  
 CC phosphatidylinositol 3-kinase (PI 3-kinase) p110 delta catalytic  
 CC subunit cDNA, using leucocyte cDNA as template. Amplified products  
 CC were used as templates in a nested PCR and the reamplified products  
 CC were then analysed using probes (see AAV31347-48) specific for p110  
 CC delta. The specific 5' RACE PCR products were combined with  
 CC partial clones #249 and M#928 to produce a composite cDNA (AAV31340)  
 CC sequence coding for human PI 3-kinase p110 delta catalytic subunit  
 CC (see AAV58570). This can be used to develop products for modulating  
 CC PI 3-kinase activity in immune system signalling and in  
 CC carcinogenesis.  
 XX

SQ Sequence 26 BP; 5 A; 8 C; 9 G; 4 T; 0 other;  
 Query Match 0.7%; Score 26; DB 19; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+04;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1500 GGAACGCTGCTCTACATGTGGCC 1525  
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 Db 26 GGAACGCTGCTCTACATGTGGCC 1

RESULT 2  
 AAX15937/c  
 ID AAX15937 standard; DNA; 26 BP.  
 XX  
 AC AAX15937;  
 XX  
 DT 14-MAY-1999 (first entry)  
 XX  
 DE PCR primer used to amplify cDNA sequence encoding p110-delta.  
 XX  
 KW Catalytic subunit; p110-delta; phosphatidylinositol 3-kinase;  
 KW PI3-kinase mediated signalling; immune system; phosphatidylinositol;  
 KW PI; kinase activity; PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN US5882910-A.  
 XX  
 PD 16-MAR-1999.  
 XX  
 PF 25-NOV-1997; 97US-0977871.  
 XX  
 PR 25-NOV-1997; 97US-0977871.  
 PR 25-NOV-1996; 96US-0777405.  
 XX  
 PA (ICOS-) ICOS CORP.  
 XX  
 PI Chantry DH, Hoekstra MF, Holtzman DA;  
 XX  
 DR WPI; 1999-214067/18.  
 XX  
 PT Novel catalytic subunits derived from phosphatidylinositol 3-kinase  
 PT enzymes - useful as antigens and for identifying agents which  
 PT modulate the enzymes kinase activity or binding to substrates and  
 PT co-factors  
 XX  
 XX Example 1; Columns 6; 22pp; English.  
 PS  
 XX PCR primers AAX15937-38 were used to isolate cDNA encoding a catalytic  
 CC subunit (p110-delta), derived from a phosphatidylinositol 3-kinase  
 CC enzyme which is involved in PI3-Kinase mediated signalling in the

CC immune system. p110-delta phosphorylates phosphatidylinositol (PI),  
 CC and derivatives of it at the 3'-hydroxyl of the inositol ring).  
 CC p110-delta may be used as an antigen in the production of  
 CC antibodies (using standard techniques) which may be used, for  
 CC example, to modulate (ie blocking, inhibiting or stimulating) the  
 CC binding between p110-delta and its binding partner. p110-delta may  
 CC also be used in assays to identify modulators which inhibit or  
 CC activate its kinase activity.  
 XX

SQ Sequence 26 BP; 5 A; 8 C; 9 G; 4 T; 0 other;  
 Query Match 0.7%; Score 26; DB 20; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+04;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1500 GGAACGCTGCTCTACATGTGGCC 1525  
 |||||  
 Db 26 GGAACGCTGCTCTACATGTGGCC 1

RESULT 3  
 AAZ32887/c  
 ID AAZ32887 standard; DNA; 26 BP.  
 XX  
 AC AAZ32887;  
 XX  
 DT 09-FEB-2000 (first entry)  
 XX  
 DE Human PI 3-kinase-related catalytic subunit p110-delta PCR primer #9.  
 XX  
 KW Lipid kinase; catalytic; subunit; p110-delta; PI 3-kinase;  
 KW phosphatidylinositol 3-kinase; heterodimeric; isoform; phosphorylation;  
 KW phosphatidylinositol (3, 4, 5) triphosphate; PIP3; activation; G protein;  
 KW cellular response; growth; differentiation; apoptosis;  
 KW phosphorylated lipid; protein kinase C; PKC; leukocyte activation;  
 KW interleukin-2; IL-2; production; T cell; leukocyte signalling; modulator;  
 KW antagonist; agonist; treatment; disorder; cell growth;  
 KW cell differentiation; immune activation; PCR; primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN US5985589-A.  
 XX  
 PD 16-NOV-1999.  
 XX  
 PF 06-JAN-1999; 99US-0225951.  
 XX  
 PR 25-NOV-1997; 97US-0977871.  
 PR 25-NOV-1996; 96US-0777405.  
 XX  
 PA (ICOS-) ICOS CORP.  
 XX  
 PI Holtzman DA, Hoekstra MF, Chantry DH;  
 XX  
 DR WPI; 2000-012785/01.  
 XX  
 PT Identifying modulators of lipid kinase subunit p110delta activity -  
 PS Example 1; Column 6; 22pp; English.  
 XX  
 CC This sequence represents human p110-delta PCR primer #9, used in the  
 CC generation of a full-length cDNA (AAZ32887) encoding a novel lipid  
 CC kinase catalytic subunit, p110-delta, related to phosphatidylinositol  
 CC 3-kinase (PI 3-kinase). PI 3-kinase is a heterodimer consisting of a  
 CC membrane-localising p85 subunit and a catalytic p110 subunit. These  
 CC subunits both have isoforms; p85 has two isoforms (alpha and beta) which  
 CC are differentially expressed, and p110 has to date three isoforms  
 CC (alpha, beta and gamma) that vary in their ability to associate with p85.  
 CC PI 3-kinase phosphorylates PI and phosphorylated derivatives of PI at  
 CC the 3' hydroxyl of the inositol ring with the primary product of PI  
 CC 3-kinase-mediated phosphorylation being phosphatidylinositol (3, 4, 5)  
 CC triphosphate (PIP3). PI 3-kinase is activated by interaction with G

CC proteins and PI 3-kinase activation is believed to be involved in a  
 CC range of cellular responses including cell growth, differentiation and  
 CC apoptosis. The downstream targets of the phosphorylated lipids generated  
 CC following PI 3-kinase activation have not been well characterised,  
 CC although some isoforms of protein kinase C (PKC) are directly activated  
 CC by PI3 in vitro. PI 3-kinase also appears to be involved in certain  
 CC aspects of leukocyte activation, such as interleukin-2 (IL-2) production  
 CC in T cells, and leukocyte signalling through G-protein coupled  
 CC receptors. p110-delta, or nucleotides encoding it, may be used to  
 CC identify modulators of p110-delta and/or PI 3-kinase activity. These may  
 CC be useful in the treatment of disorders associated with cell growth,  
 CC cell differentiation, apoptosis or immune activation.

XX Sequence 26 BP; 5 A; 8 C; 9 G; 4 T; 0 other;

Query Match 0.7%; Score 26; DB 21; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+04;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1500 GGGACGCTGCCTCTACATGCGGCC 1525

DB 26 GGGACGCTGCCTCTACATGCGGCC 1

#### RESULT 4

AAV31346/C

ID AAV31346 standard; DNA; 25 BP.

XX AAV31346;

XX 12-OCT-1998 (first entry)

XX Phosphatidylinositol 3-kinase p110 delta subunit RACE primer.

XX Phosphatidylinositol 3-kinase; p110 delta; human; immune system;

KW carcinogenesis; diagnosis; PCR; primer; RACE; ss.

OS Synthetic.

OS Homo sapiens.

XX WO9823760-A1.

XX 04-JUN-1998.

XX 25-NOV-1997; 97WO-US21655.

XX 25-NOV-1996; 96US-0777405.

XX (ICOS-) ICOS CORP.

XX Chantry DH, Hoekstra MF, Holtzman DA;

XX WPI; 1998-322736/28.

XX New phosphatidylinositol 3-kinase catalytic subunit - used to  
 PT develop products for modulating kinase activity in immune system  
 PT signalling and in carcinogenesis

PS Example 1; Page 11; 53pp; English.

XX 2 Antisense gene-specific oligonucleotide primers (see AAV31345 and  
 CC AAV31346) respectively comprise a primary RACE primer and a nested  
 CC RACE primer, and are based on the 5' end of M928, a cDNA clone  
 CC obtained from human macrophage cDNA by PCR amplification (see  
 CC AAV31343-44). They were used to amplify 5' sequences of human  
 CC phosphatidylinositol 3-kinase (PI 3-kinase) p110 delta catalytic  
 CC subunit cDNA, using leucocyte cDNA as template. Amplified products  
 CC were used as templates in a nested PCR and the reamplified products  
 CC were then analysed using probes (see AAV31347-48) specific for p110  
 CC delta. The specific 5' RACE PCR products were combined with  
 CC partial clones #249 and M928 to produce a composite cDNA (AAV31340)  
 CC sequence coding for human PI 3-kinase p110 delta catalytic subunit  
 CC (see AAW58570). This can be used to develop products for modulating

CC PI 3-kinase activity in immune system signalling and in  
 CC carcinogenesis.

XX Sequence 25 BP; 4 A; 9 C; 10 G; 2 T; 0 other;

Query Match 0.6%; Score 25; DB 19; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+04;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1435 GCGGACTGCCCCATTGCTGGGCC 1459

DB 25 GCGGACTGCCCCATTGCTGGGCC 1

#### RESULT 5

AAV15938/C

ID AAV15938 standard; DNA; 25 BP.

XX AAV15938;

XX 14-MAY-1999 (first entry)

XX PCR primer used to amplify cDNA sequence encoding p110-delta.

XX Catalytic subunit; p110-delta; phosphatidylinositol 3-kinase;

KW PI3-Kinase mediated signalling; immune system; phosphatidylinositol;

KW PI; kinase activity; PCR primer; ss.

XX Synthetic.

OS Homo sapiens.

XX US5882910-A.

XX 16-MAR-1999.

XX 25-NOV-1997; 97US-0977871.

XX 25-NOV-1997; 97US-0977871.

XX 25-NOV-1996; 96US-0777405.

XX (ICOS-) ICOS CORP.

XX Chantry DH, Hoekstra MF, Holtzman DA;

XX WPI; 1999-214067/18.

XX Novel catalytic subunits derived from phosphatidylinositol 3-kinase  
 PT enzymes - useful as antigens and for identifying agents which  
 PT modulate the enzymes kinase activity or binding to substrates and  
 PT co-factors

PS Example 1; Columns 6; 22pp; English.

XX PCR primers AAV15937-38 were used to isolate cDNA encoding a catalytic  
 CC subunit (p110-delta), derived from a Phosphatidylinositol 3-kinase  
 CC enzyme which is involved in PI3-Kinase mediated signalling in the  
 CC immune system. p110-delta phosphorylates phosphatidylinositol (PI),  
 CC and derivatives of it at the 3'-hydroxyl of the inositol ring).  
 CC p110-delta may be used as an antigen in the production of  
 CC antibodies (using standard techniques) which may be used, for  
 CC example, to modulate (ie blocking, inhibiting or stimulating) the  
 CC binding between p110-delta and its binding partner. p110-delta may  
 CC also be used in assays to identify modulators which inhibit or  
 CC activate its kinase activity.

XX Sequence 25 BP; 4 A; 9 C; 10 G; 2 T; 0 other;

Query Match 0.6%; Score 25; DB 20; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+04;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1435 GCGGACTGCCCCATTGCTGGGCC 1459

|||||







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PT modulate the enzymes kinase activity or binding to substrates and
PT co-factors
XX
PS Example 1; Columns 7; 22pp; English.
XX
CC Probes AX15939-40 were used to isolate cDNA encoding a catalytic
CC subunit (p110-delta), derived from a phosphatidylinositol 3-kinase
CC enzyme system. PI3-kinase mediated signalling in the
CC immune system. p110-delta phosphorylates phosphatidylinositol (PI),
CC and derivatives of it at the 3'-hydroxyl of the inositol ring).
CC p110-delta may be used as an antigen in the production of
CC antibodies (using standard techniques) which may be used, for
CC example, to modulate (ie blocking, inhibiting or stimulating) the
CC binding between p110-delta and its binding partner. p110-delta may
CC also be used in assays to identify modulators which inhibit or
CC activate its kinase activity.
XX
SQ Sequence 23 BP; 8 A; 7 C; 8 G; 0 U; 0 other;
    Query Match      0.6%; Score 23; DB 20; Length 23;
    Best Local Similarity 100.0%; Pred. No. 1.4e+05;
    Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1132 CTCGTGTCCCTGTGTCCTGG 1154
Db 23 CTCGTGTCCCTGTGTCCTGG 1

RESULT 11
AAZ32889/c
ID AAZ32889 standard; DNA; 23 BP.
XX
AC AAZ32889;
XX
DT 09-FEB-2000 (first entry)
DE Human PI 3-kinase-related catalytic subunit p110-delta PCR primer #11.
XX
KW Lipid kinase; catalytic; subunit; p110-delta; PI 3-kinase;
KW phosphatidylinositol 3-kinase; heterodimeric; isoform; phosphorylation;
KW phosphatidylinositol (3, 4, 5) triphosphate; PIP3; activation; G protein;
KW cellular response; growth; differentiation; apoptosis;
KW phosphorylated lipid; protein kinase C; PKC; leukocyte activation;
KW interleukin-2; IL-2; production; T cell; leukocyte signalling; modulator;
KW antagonist; agonist; treatment; disorder; cell growth;
KW cell differentiation; immune activation; PCR; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5985589-A.
PD 16-NOV-1999.
XX
PF 06-JAN-1999; 99US-0225951.
XX
PR 25-NOV-1997; 97US-0977871.
PR 25-NOV-1996; 96US-0777405.
XX
PA (ICOS-) ICOS CORP.
XX
PI Holtzman DA, Hoekstra MF, Chantry DH;
XX
DR WPI; 2000-012785/01.
XX
PT Identifying modulators of lipid kinase subunit p110delta activity -
PS Example 1; Column 7; 22pp; English.
XX
CC This sequence represents human p110-delta PCR primer #11, used in the
CC generation of a full-length cDNA (AAZ32882) encoding a novel lipid
CC kinase catalytic subunit, p110-delta, related to phosphatidylinositol
CC 3-kinase (PI 3-kinase). PI 3-kinase is a heterodimer consisting of a

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CC membrane-localising p85 subunit and a catalytic p110 subunit. These
CC subunits both have isoforms; p85 has two isoforms (alpha and beta) which
CC are differentially expressed, and p110 has to date three isoforms
CC (alpha, beta and gamma) that vary in their ability to associate with p85.
CC PI 3-kinase phosphorylates PI and phosphorylated derivatives of PI at
CC the 3' hydroxyl of the inositol ring with the primary product of PI
CC 3-kinase-mediated phosphorylation being phosphatidylinositol (3, 4, 5)
CC triphosphate (PIP3). PI 3-kinase is activated by interaction with G
CC proteins and PI 3-kinase activation is believed to be involved in a
CC range of cellular responses including cell growth, differentiation and
CC apoptosis. The downstream targets of the phosphorylated lipids generated
CC following PI 3-kinase activation have not been well characterised,
CC although some isoforms of protein kinase C (PKC) are directly activated
CC by PIP3 in vitro. PI 3-kinase also appears to be involved in certain
CC aspects of leukocyte activation, such as interleukin-2 (IL-2) production
CC in T cells, and leukocyte signalling through G-protein coupled
CC receptors. p110-delta, or nucleotides encoding it, may be used to
CC identify modulators of p110-delta and/or PI 3-kinase activity. These may
CC be useful in the treatment of disorders associated with cell growth,
CC cell differentiation, apoptosis or immune activation.
XX
SQ Sequence 23 BP; 4 A; 6 C; 10 G; 3 T; 0 other;
    Query Match      0.6%; Score 23; DB 21; Length 23;
    Best Local Similarity 100.0%; Pred. No. 1.4e+05;
    Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1149 CCTGGAGCAGCGTTCGCATC 1171
Db 23 CCTGGAGCAGCGTTCGCATC 1

RESULT 12
AAZ32890/c
ID AAZ32890 standard; DNA; 23 BP.
XX
AC AAZ32890;
XX
DT 09-FEB-2000 (first entry)
DE Human PI 3-kinase-related catalytic subunit p110-delta PCR primer #12.
XX
KW Lipid kinase; catalytic; subunit; p110-delta; PI 3-kinase;
KW phosphatidylinositol 3-kinase; heterodimeric; isoform; phosphorylation;
KW phosphatidylinositol (3, 4, 5) triphosphate; PIP3; activation; G protein;
KW cellular response; growth; differentiation; apoptosis;
KW phosphorylated lipid; protein kinase C; PKC; leukocyte activation;
KW interleukin-2; IL-2; production; T cell; leukocyte signalling; modulator;
KW antagonist; agonist; treatment; disorder; cell growth;
KW cell differentiation; immune activation; PCR; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5985589-A.
PD 16-NOV-1999.
XX
PF 06-JAN-1999; 99US-0225951.
XX
PR 25-NOV-1997; 97US-0977871.
PR 25-NOV-1996; 96US-0777405.
XX
PA (ICOS-) ICOS CORP.
XX
PI Holtzman DA, Hoekstra MF, Chantry DH;
XX
DR WPI; 2000-012785/01.
XX
PT Identifying modulators of lipid kinase subunit p110delta activity -
PS Example 1; Column 7; 22pp; English.
XX

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CC This sequence represents human p110-delta PCR primer #12, used in the  
CC generation of a full-length cDNA (AAZ32882) encoding a novel lipid  
CC kinase catalytic subunit, p110-delta, related to phosphatidylinositol  
CC 3-kinase (PI 3-kinase). PI 3-kinase is a heterodimer consisting of a  
CC membrane-localising p85 subunit and a catalytic p110 subunit. These  
CC subunits both have isoforms; p85 has two isoforms (alpha and beta) which  
CC are differentially expressed, and p110 has to date three isoforms  
CC (alpha, beta and gamma) that vary in their ability to associate with p85.  
CC PI 3-kinase phosphorylates PI and phosphorylated derivatives of PI at  
CC the 3' hydroxyl of the inositol ring with the primary product of PI at  
CC 3-kinase-mediated phosphorylation being phosphatidylinositol (3, 4, 5)  
CC triphosphate (PIP3). PI 3-kinase is activated by interaction with G  
CC proteins and PI 3-kinase activation is believed to be involved in a  
CC range of cellular responses including cell growth, differentiation and  
CC apoptosis. The downstream targets of the phosphorylated lipids generated  
CC following PI 3-kinase activation have not been well characterised,  
CC although some isoforms of protein kinase C (PKC) are directly activated  
CC by PIP3 in vitro. PI 3-kinase also appears to be involved in certain  
CC aspects of leukocyte activation, such as interleukin-2 (IL-2) production  
CC in T cells, and leukocyte signalling through G-protein coupled  
CC receptors. p110-delta, or nucleotides encoding it, may be used to  
CC identify modulators of p110-delta and/or PI 3-kinase activity. These may  
CC be useful in the treatment of disorders associated with cell growth,  
CC cell differentiation, apoptosis or immune activation.

XX Sequence 23 BP; 8 A; 7 C; 8 G; 0 U; 0 other;

Query Match 0.6%; Score 23; DB 21; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1132 CTCGTGTCCTGTCCTGTCCTGG 1154

DB 23 CTCGTGTCCTGTCCTGTCCTGG 1

RESULT 13

AAV31350/c

ID AAV31350 standard; DNA; 22 BP.

XX AAV31350;

XX 12-OCT-1998 (first entry)

XX Phosphatidylinositol 3-kinase p110 delta subunit primer.

DE Phosphatidylinositol 3-kinase; p110 delta; human; immune system;

KW carcinogenesis; diagnosis; PCR; primer; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9823760-A1.

PN 04-JUN-1998.

XX 25-NOV-1997; 97WO-US21655.

XX 25-NOV-1996; 96US-0777405.

XX (ICOS-) ICOS CORP.

XX Chantry DH, Hoekstra MF, Holtzman DA;

XX WPI; 1998-322736/28.

XX New phosphatidylinositol 3-kinase catalytic subunit - used to  
PT develop products for modulating kinase activity in immune system  
PT signalling and in carcinogenesis

XX Example 1; Page 12; 53pp; English.

XX This 3' primer was used with a 5' primer (see AAV31349) in the PCR

CC amplification of 5'RACE PCR products (see AAV31345-46) of human  
CC leukocyte cDNA. The 5' primer includes a 5' BamHI site and  
CC sequences that code for a FLAG peptide (see AAW58571) which is  
CC recognised by the M2 anti-FLAG monoclonal antibody. The PCR  
CC product was combined with restriction fragments of partial clones  
CC #249 and M#928 to produce a full-length cDNA (see AAV31347) for the  
CC p100 delta catalytic subunit (see AAW58570) of human  
CC phosphatidylinositol 3-kinase (PI 3-kinase). This was incorporated  
CC into expression vector pcDNA3, and FLAG-tagged p110 delta was  
CC expressed in transfected COS cells. p110 delta can be used to  
CC develop products for modulating PI 3-kinase activity in immune  
CC system signalling and in carcinogenesis.

XX Sequence 22 BP; 5 A; 7 C; 6 G; 4 T; 0 other;

Query Match 0.6%; Score 22; DB 19; Length 22;

Best Local Similarity 100.0%; Pred. No. 2.2e+05;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1501 GGAACGCTGCCTCTACATGTGG 1522

DB 22 GGAACGCTGCCTCTACATGTGG 1

RESULT 14

AAV15942/c

ID AAV15942 standard; DNA; 22 BP.

XX AAV15942;

XX 14-MAY-1999 (first entry)

XX PCR primer used to amplify cDNA sequence encoding p110-delta.

DE Catalytic subunit; p110-delta; phosphatidylinositol 3-kinase;

KW PI3-Kinase mediated signalling; immune system; phosphatidylinositol;

KW PI; kinase activity; PCR primer; ss.

XX Synthetic.

OS Homo sapiens.

XX US5882910-A.

XX 16-MAR-1999.

XX 25-NOV-1997; 97US-0977871.

XX 25-NOV-1997; 97US-0977871.

PR 25-NOV-1996; 96US-0777405.

XX (ICOS-) ICOS CORP.

XX Chantry DH, Hoekstra MF, Holtzman DA;

XX WPI; 1999-214067/18.

XX Novel catalytic subunits derived from phosphatidylinositol 3-kinase  
PT enzymes - useful as antigens and for identifying agents which  
PT modulate the enzymes kinase activity or binding to substrates and  
PT co-factors

XX Example 1; Columns 7; 22pp; English.

XX PCR primers AAV15941-42 were used to isolate cDNA encoding a catalytic  
CC subunit (p110-delta), derived from a Phosphatidylinositol 3-kinase  
CC enzyme which is involved in PI3-Kinase mediated signalling in the  
CC immune system. p110-delta phosphorylates phosphatidylinositol (PI),  
CC and derivatives of it at the 3'-hydroxyl of the inositol ring.

CC p110-delta may be used as an antigen in the production of

CC antibodies (using standard techniques) which may be used, for

CC example, to modulate (ie blocking, inhibiting or stimulating) the

CC binding between p110-delta and its binding partner. p110-delta may

CC also be used in assays to identify modulators which inhibit or

CC activate its kinase activity.  
XX  
SQ Sequence 22 BP; 5 A; 7 C; 6 G; 4 T; 0 other;  
Query Match 0.6%; Score 22; DB 20; Length 22;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1501 GGAACGCTGCCTCTACATGTGG 1522  
Db 22 GGAACGCTGCCTCTACATGTGG 1  
RESULT 15  
ID AAZ32892/c  
XX AAZ32892 standard; DNA; 22 BP.  
AC AAZ32892;  
XX  
DT 09-FEB-2000 (first entry)  
XX  
DE Human PI 3-kinase-related catalytic subunit p110-delta PCR primer #14.  
XX  
KW Lipid kinase; catalytic; subunit; p110-delta; PI 3-kinase;  
KW phosphatidylinositol 3-kinase; heterodimeric; isoform; phosphorylation;  
KW phosphatidylinositol (3, 4, 5) triphosphate; PIP3; activation; G protein;  
KW cellular response; growth; differentiation; apoptosis;  
KW phosphorylated lipid; protein kinase C; PKC; leukocyte activation;  
KW interleukin-2; IL-2; production; T cell; leukocyte signalling; modulator;  
KW antagonist; agonist; treatment; disorder; cell growth;  
KW cell differentiation; immune activation; PCR; primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN US5985589-A.  
XX 16-NOV-1999.  
PD  
XX  
PF 06-JAN-1999; 99US-0225951.  
XX  
PR 25-NOV-1997; 97US-0977871.  
PR 25-NOV-1996; 96US-0777405.  
XX  
PA (ICOS-) ICOS CORP.  
XX  
PI Holtzman DA, Hoekstra MF, Chantry DH;  
XX  
DR WPI; 2000-012785/01.  
XX  
PT Identifying modulators of lipid kinase subunit p110delta activity -  
XX  
PS Example 1; Column 7; 22pp; English.  
XX  
CC This sequence represents human p110-delta PCR primer #14, used in the  
CC generation of a full-length cDNA (AAZ32882) encoding a novel lipid  
CC kinase catalytic subunit, p110-delta, related to phosphatidylinositol  
CC 3-kinase (PI 3-kinase). PI 3-kinase is a heterodimer consisting of a  
CC membrane-localising p85 subunit and a catalytic p110 subunit. These  
CC subunits both have isoforms; p85 has two isoforms (alpha and beta) which  
CC are differentially expressed, and p110 has to date three isoforms  
CC (alpha, beta and gamma) that vary in their ability to associate with p85.  
CC PI 3-kinase phosphorylates PI and phosphorylated derivatives of PI at  
CC the 3' hydroxyl of the inositol ring with the primary product of PI  
CC 3-kinase-mediated phosphorylation being phosphatidylinositol (3, 4, 5)  
CC triphosphate (PIP3). PI 3-kinase is activated by interaction with G  
CC proteins and PI 3-kinase activation is believed to be involved in a  
CC range of cellular responses including cell growth, differentiation and  
CC apoptosis. The downstream targets of the phosphorylated lipids generated  
CC following PI 3-kinase activation have not been well characterised,  
CC although some isoforms of protein kinase C (PKC) are directly activated  
CC by PIP3 in vitro. PI 3-kinase also appears to be involved in certain  
CC aspects of leukocyte activation, such as interleukin-2 (IL-2) production

CC in T cells, and leukocyte signalling through G-protein coupled  
CC receptors, p110-delta, or nucleotides encoding it, may be used to  
CC identify modulators of p110-delta and/or PI 3-kinase activity. These may  
CC be useful in the treatment of disorders associated with cell growth,  
CC cell differentiation, apoptosis or immune activation.  
XX  
SQ Sequence 22 BP; 5 A; 7 C; 6 G; 4 T; 0 other;  
Query Match 0.6%; Score 22; DB 21; Length 22;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1501 GGAACGCTGCCTCTACATGTGG 1522  
Db 22 GGAACGCTGCCTCTACATGTGG 1  
Search completed: March 3, 2003, 20:12:24  
Job time : 741 secs

GenCore version 5.1.4\_p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2003, 19:58:31 ; Search time 135 Seconds  
(without alignments)  
8786.857 Million cell updates/sec

Title: US-10-049-743-1  
Perfect score: 3868  
Sequence: 1 gaattcgacagcgccg.....ggtcttggtacagaattc 3868

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 452144

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA.\*  
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2: /cgn2.6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2.6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2.6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2.6/ptodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2.6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match	Length	ID	Description	
C 1	26	0.7	26	2	US-08-777-405A-9	Sequence 9, Appli
C 2	26	0.7	26	2	US-08-777-871A-9	Sequence 9, Appli
C 3	26	0.7	26	2	US-09-225-951-9	Sequence 9, Appli
C 4	25	0.6	25	2	US-08-777-405A-10	Sequence 10, Appl
C 5	25	0.6	25	2	US-08-777-871A-10	Sequence 10, Appl
C 6	25	0.6	25	2	US-09-225-951-10	Sequence 10, Appl
C 7	23	0.6	23	2	US-08-777-405A-11	Sequence 11, Appl
C 8	23	0.6	23	2	US-08-777-405A-12	Sequence 12, Appl
C 9	23	0.6	23	2	US-08-777-871A-11	Sequence 11, Appl
C 10	23	0.6	23	2	US-08-777-871A-12	Sequence 12, Appl
C 11	23	0.6	23	2	US-09-225-951-11	Sequence 11, Appl
C 12	23	0.6	23	2	US-09-225-951-12	Sequence 12, Appl
C 13	22	0.6	22	2	US-08-777-405A-14	Sequence 14, Appl
C 14	22	0.6	22	2	US-08-777-871A-14	Sequence 14, Appl
C 15	22	0.6	22	2	US-09-225-951-14	Sequence 14, Appl
C 16	21	0.5	21	2	US-08-777-405A-7	Sequence 7, Appli
C 17	21	0.5	21	2	US-08-777-405A-8	Sequence 8, Appli
C 18	21	0.5	21	2	US-08-777-405A-16	Sequence 16, Appl
C 19	21	0.5	21	2	US-08-777-871A-7	Sequence 7, Appli
C 20	21	0.5	21	2	US-08-777-871A-8	Sequence 8, Appli
C 21	21	0.5	21	2	US-08-777-871A-16	Sequence 16, Appl
C 22	21	0.5	21	2	US-09-225-951-7	Sequence 7, Appli
C 23	21	0.5	21	2	US-09-225-951-8	Sequence 8, Appli
C 24	21	0.5	21	2	US-09-225-951-16	Sequence 16, Appl
C 25	21	0.5	21	3	US-09-357-070-3	Sequence 3, Appli
C 26	20	0.5	20	3	US-09-357-070-8	Sequence 8, Appli
C 27	20	0.5	20	3	US-09-357-070-9	Sequence 9, Appli

C 28	20	0.5	20	3	US-09-357-070-10	Sequence 10, Appl
C 29	20	0.5	20	3	US-09-357-070-11	Sequence 11, Appl
C 30	20	0.5	20	3	US-09-357-070-12	Sequence 12, Appl
C 31	20	0.5	20	3	US-09-357-070-13	Sequence 13, Appl
C 32	20	0.5	20	3	US-09-357-070-14	Sequence 14, Appl
C 33	20	0.5	20	3	US-09-357-070-15	Sequence 15, Appl
C 34	20	0.5	20	3	US-09-357-070-16	Sequence 16, Appl
C 35	20	0.5	20	3	US-09-357-070-17	Sequence 17, Appl
C 36	20	0.5	20	3	US-09-357-070-18	Sequence 18, Appl
C 37	20	0.5	20	3	US-09-357-070-19	Sequence 19, Appl
C 38	20	0.5	20	3	US-09-357-070-20	Sequence 20, Appl
C 39	20	0.5	20	3	US-09-357-070-21	Sequence 21, Appl
C 40	20	0.5	20	3	US-09-357-070-22	Sequence 22, Appl
C 41	20	0.5	20	3	US-09-357-070-23	Sequence 23, Appl
C 42	20	0.5	20	3	US-09-357-070-24	Sequence 24, Appl
C 43	20	0.5	20	3	US-09-357-070-25	Sequence 25, Appl
C 44	20	0.5	20	3	US-09-357-070-26	Sequence 26, Appl
C 45	20	0.5	20	3	US-09-357-070-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1  
US-08-777-405A-9/C  
; Sequence 9, Application US/08777405A  
; Patent No. 5858753  
; GENERAL INFORMATION:  
; APPLICANT: Chantry, David  
; APPLICANT: Hoekstra, Merl F.  
; APPLICANT: Holtzman, Douglas A  
; TITLE OF INVENTION: No. 5858753el Lipid Kinase  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
; STREET: 6300 Sears Tower/233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/777,405A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5858753and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/33441  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
US-08-777-405A-9  
Query Match 0.7%; Score 26; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1500 GGGACGCTGCTCTACATGTGGCCC 1525  
Db 26 GGGACGCTGCTCTACATGTGGCCC 1

RESULT 2  
US-08-977-871A-9/c  
; Sequence 9, Application US/08977871A  
; Patent No. 5882910  
; GENERAL INFORMATION:  
; APPLICANT: Chantry, David  
; APPLICANT: Hoekstra, Merl F.  
; APPLICANT: Holtzman, Douglas A  
; TITLE OF INVENTION: No. 5882910el Lipid Kinase  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
; STREET: 6300 Sears Tower/233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/977,871A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/777,405  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5882910and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/33441  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
US-08-977-871A-9  
Query Match 0.7%; Score 26; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 26; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
QY 1500 GGAACGCTGCTCTACATGTGGCC 1525  
Db 26 GGAACGCTGCTCTACATGTGGCC 1  
RESULT 3  
US-09-225-951-9/c  
; Sequence 9, Application US/09225951  
; Patent No. 5985589  
; GENERAL INFORMATION:  
; APPLICANT: Chantry, David  
; APPLICANT: Hoekstra, Merl F.  
; APPLICANT: Holtzman, Douglas A  
; TITLE OF INVENTION: No. 5985589el Lipid Kinase  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
; STREET: 6300 Sears Tower/233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA

; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/225,951  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5985589and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/33441  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
US-09-225-951-9  
Query Match 0.7%; Score 26; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 26; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
QY 1500 GGAACGCTGCTCTACATGTGGCC 1525  
Db 26 GGAACGCTGCTCTACATGTGGCC 1  
RESULT 4  
US-08-777-405A-10/c  
; Sequence 10, Application US/08777405A  
; Patent No. 5858753  
; GENERAL INFORMATION:  
; APPLICANT: Chantry, David  
; APPLICANT: Hoekstra, Merl F.  
; APPLICANT: Holtzman, Douglas A  
; TITLE OF INVENTION: No. 5858753el Lipid Kinase  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
; STREET: 6300 Sears Tower/233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/777,405A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5858753and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/33441  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-777-405A-10

Query Match
Best Local Similarity 100.0%; Score 25; DB 2; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1435 GCGGAGCTGCCCATTCCTGGGCC 1459
|||||
DB 25 GCGGAGCTGCCCATTCCTGGGCC 1

RESULT 5
US-08-777-871A-10/c
; Sequence 10, Application US/08977871A
; Patent No. 5882910
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5882910el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,871A
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5882910and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-777-871A-10

Query Match
Best Local Similarity 100.0%; Score 25; DB 2; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1435 GCGGAGCTGCCCATTCCTGGGCC 1459
|||||
DB 25 GCGGAGCTGCCCATTCCTGGGCC 1

RESULT 6
US-09-225-951-10/c
; Sequence 10, Application US/09225951
; Patent No. 5858753
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5858753el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,405A
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5882910and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-777-871A-10

Query Match
Best Local Similarity 100.0%; Score 25; DB 2; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1435 GCGGAGCTGCCCATTCCTGGGCC 1459
|||||
DB 25 GCGGAGCTGCCCATTCCTGGGCC 1

RESULT 7
US-08-777-405A-11/c
; Sequence 11, Application US/08777405A
; Patent No. 5858753
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5858753el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,405A
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5882910and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-777-871A-10

Query Match
Best Local Similarity 100.0%; Score 25; DB 2; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1435 GCGGAGCTGCCCATTCCTGGGCC 1459
|||||
DB 25 GCGGAGCTGCCCATTCCTGGGCC 1

RESULT 8
US-08-777-405A-12/c
; Sequence 12, Application US/08777405A
; Patent No. 5858753
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5858753el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,405A
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5882910and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-777-871A-10

Query Match
Best Local Similarity 100.0%; Score 25; DB 2; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1435 GCGGAGCTGCCCATTCCTGGGCC 1459
|||||
DB 25 GCGGAGCTGCCCATTCCTGGGCC 1

RESULT 9
US-08-777-405A-13/c
; Sequence 13, Application US/08777405A
; Patent No. 5858753
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5858753el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,405A
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5882910and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-777-871A-10

Query Match
Best Local Similarity 100.0%; Score 25; DB 2; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1435 GCGGAGCTGCCCATTCCTGGGCC 1459
|||||
DB 25 GCGGAGCTGCCCATTCCTGGGCC 1

RESULT 10
US-08-777-405A-14/c
; Sequence 14, Application US/08777405A
; Patent No. 5858753
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5858753el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,405A
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5882910and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-777-871A-10

Query Match
Best Local Similarity 100.0%; Score 25; DB 2; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1435 GCGGAGCTGCCCATTCCTGGGCC 1459
|||||
DB 25 GCGGAGCTGCCCATTCCTGGGCC 1

RESULT 11
US-08-777-405A-15/c
; Sequence 15, Application US/08777405A
; Patent No. 5858753
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5858753el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,405A
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5882910and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 10:

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;
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5858753and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
;
US-08-777-405A-11
;
Query Match 0.6%; Score 23; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 CCCTGGAGCAGCGTTCGCGATC 1171
Db 23 CCCTGGAGCAGCGTTCGCGATC 1

RESULT 8
US-08-777-405A-12/c
; Sequence 12, Application US/08777405A
; Patent No. 5858753
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5858753el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,405A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/777,405
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5858753and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
;
US-08-777-405A-11
;
Query Match 0.6%; Score 23; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 CCCTGGAGCAGCGTTCGCGATC 1171
Db 23 CCCTGGAGCAGCGTTCGCGATC 1

RESULT 10
US-08-777-871A-11/c
; Sequence 11, Application US/08977871A
; Patent No. 5882910
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5882910el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,871A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/777,405
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5882910and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
;
US-08-977-871A-11
;
Query Match 0.6%; Score 23; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 CCCTGGAGCAGCGTTCGCGATC 1171
Db 23 CCCTGGAGCAGCGTTCGCGATC 1

RESULT 10
US-08-977-871A-12/c
; Sequence 12, Application US/08977871A
; Patent No. 5882910
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5882910el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,405A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5858753and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
;
US-08-777-405A-12
;
Query Match 0.6%; Score 23; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1132 CTCTGTGTCCCTGTGTGGTCCCTGG 1154
Db 23 CTCTGTGTCCCTGTGTGGTCCCTGG 1

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,871A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/777,405
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5882910and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; US-08-977-871A-12

Query Match 0.6%; Score 23; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1132 CTCGTGTCCTGTGGTCCCTGG 1154
DB 23 CTCGTGTCCTGTGGTCCCTGG 1

RESULT 11
; Sequence 11, Application US/09225951
; Patent No. 5985589
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5985589el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,951
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5985589and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; US-09-225-951-12

Query Match 0.6%; Score 23; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1132 CTCGTGTCCTGTGGTCCCTGG 1154
DB 23 CTCGTGTCCTGTGGTCCCTGG 1
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; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; US-09-225-951-11

Query Match 0.6%; Score 23; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 CCTGGAGCAGCGCTTCCGCATC 1171
DB 23 CCTGGAGCAGCGCTTCCGCATC 1

RESULT 12
; Sequence 12, Application US/09225951
; Patent No. 5985589
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5985589el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,951
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5985589and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; US-09-225-951-12

Query Match 0.6%; Score 23; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1132 CTCGTGTCCTGTGGTCCCTGG 1154
DB 23 CTCGTGTCCTGTGGTCCCTGG 1
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; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
US-09-225-951-14

Query Match 0.6%; Score 22; DB 2; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.8e+04;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 22 GGAACGCTGCCTCTACATGTGG 1

Search completed: March 4, 2003, 06:27:43  
Job time : 136 secs



GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 3, 2003, 20:00:22 ; Search time 1105 Seconds  
(without alignments)  
2338.022 Million cell updates/sec

Title: US-10-049-743-1  
Perfect score: 3868  
Sequence: 1 caattcgcacagccgccc.....gatcttgatcacgaattc 3868

Scoring table: IDENTITY\_NUC  
Gapop 10.0 : Gapext 1.0

Searched: 478924 seqs, 333959956 residues  
Total number of hits satisfying chosen parameters: 200426

Minimum	DB seq	length: 0
Maximum	DB seq	length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 s

Database :	Published_Applications_NA:**
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2:	/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
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4:	/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
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6:	/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	20	0.5	30	10	US-09-494-438-1	Sequence 1, Appli
C 2	18.6	0.5	29	10	US-09-996-606-4	Sequence 4, Appli
C 3	17.6	0.5	25	10	US-09-866-108-3779	Sequence 3779, Ap
C 5	17.6	0.5	25	10	US-09-866-108-3780	Sequence 3780, Ap
C 6	17.4	0.4	28	10	US-09-894-633A-20	Sequence 20, Appl
C 7	17.4	0.4	30	10	US-09-791-171-160	Sequence 160, App
C 8	17.2	0.4	22	9	US-09-804-171A-16	Sequence 16, Appl
C 9	17	0.4	25	10	US-09-866-108-3764	Sequence 3764, Ap
C 10	17	0.4	25	10	US-09-866-108-3778	Sequence 3778, Ap
C 11	17	0.4	25	10	US-09-866-108-3895	Sequence 3895, Ap
C 12	17	0.4	25	10	US-09-866-108-3945	Sequence 3945, Ap
C 13	17	0.4	25	10	US-09-866-108-4394	Sequence 4394, Ap
C 14	17	0.4	25	10	US-09-866-108-4395	Sequence 4395, Ap
C 15	17	0.4	25	10	US-09-866-108-12035	Sequence 12035, A
C 16	17	0.4	25	10	US-09-866-108-12894	Sequence 12894, A
C 17	17	0.4	25	10	US-09-866-108-12896	Sequence 12896, A
C 18	17	0.4	25	10	US-09-866-108-12897	Sequence 12897, A
C 19	17	0.4	25	10	US-09-866-108-12898	Sequence 12898, A
C 20	17	0.4	25	10	US-09-866-108-12899	Sequence 12899, A

## AI.TIGNMENTS

## RESULT 1

US-09-494-438-1/c

03 03 434 438 17C  
: Sequence 1. Application US/09494438

: Patent No. US20020037504A1

GENERAL INFORMATION:

GENERAL INFORMATION: ARAHTRA. MASAOMI

APPLICANT: ARAHINA, MASAO  
APPLICANT: FUKUZAWA, CHIKAFUSA

APPLICANT: FUKUZAWA, CHIKAFUSA  
TITLE OF INVENTION: METHOD FOR PREPARING TEMPLATE DNA FROM PROCESSED  
VEGETABLE FOOD, WHICH IS FEASIBLE FOR AMPLIFICATION OF  
DNA REGION BY PCR METHOD

: FILE REFERENCE: 8361-0011-0

FILE REFERENCE: 0001 0011 0  
CURRENT APPLICATION NUMBER: US/09/494.438

; CURRENT AFFIDAVIT NUMBER: 05/05/454,45  
 : CURRENT FILING DATE: 2000-01-31

: PRIOR APPLICATION NUMBER: 2000

: PRIOR FILING DATE: 1999-11-  
 : PRIOR AFFILIATION NUMBER: 5

NUMBER OF S

: NUMBER OF :  
: SOFTWARE:: SOFTWARE.  
: SEO ID NO 1

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, SEQ ID NO: 1
: LENGTH: 30

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LENGTH: 30  
TYPE: DNA

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: LIFE: DNA
:
: ORGANISM: Artificial Sequence
:
: FEATURE:
:
: OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA

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Query Match 0.58; Score 20; DB 10; Length 30;

Query Match  
Best Local Similarity

Best local similarity 02.10, seq: no: 0.00007  
Matches 23: Conservative 0: Mismatches 5: Indels

QY 2688 CAGACACCATTCGCCAACATCCAACTCAA 2715

QY 2088 CAGACACCAICGCGCAACATCCAACTCA

## RESULT 2

US-09-996-606-4/c

: Sequence 4. Application US/09996606

: Patent No. US20020127653A1

GENERAL IN-  
PATIENT NO. 0

GENERAL INFORMATION: DANIEL R. SOPPET. DANIEL R. SOPPET.

RUHEN. STEVEN M.

ROBEN, STEVEN M.  
TITLE OF INVENTION: HEMATOPOIETIC SIGNALING FACTOR

NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNER, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: US  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/996,606  
FILING DATE: 30-No. US20020127653A1-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/008,490  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: STEFFE, ERIC K  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.0600001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-996-606-4

Query Match 0.5%; Score 18.6; DB 10; Length 29;  
Best Local Similarity 84.0%; Pred. No. 1.7e+05;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3356 AGAGGAGCGGCTCGGGTCGCGG 3380  
Db 27 AGTGGAGCGCGCGCGGTCGACGG 3

RESULT 3  
US-09-866-108-3779  
; Sequence 3779, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharon G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30

; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 3779  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-3779

Query Match 0.5%; Score 17.6; DB 10; Length 25;  
Best Local Similarity 83.3%; Pred. No. 2.8e+05;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2322 CCCAGCACCAAGGAGCTGATGCAC 2345  
Db 2 CCCAGGCCAAGGAACGTGGCAC 25

RESULT 4  
US-09-866-108-3780  
; Sequence 3780, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharon G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 3780  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-3780

Query Match 0.5%; Score 17.6; DB 10; Length 25;  
Best Local Similarity 83.3%; Pred. No. 2.8e+05;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2322 CCCAGACCAAGGAGCTGATGCAC 2345  
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Db 1 CCCAGGCCAAGGAAGCTGGCACT 24

RESULT 5  
US-09-894-633A-20/c  
; Sequence 20, Application US/09894633A  
; Patent No. US20020124285A1  
; GENERAL INFORMATION:  
; APPLICANT: Conner, Timothy  
; APPLICANT: Dubois, Patrice  
; APPLICANT: Malven, Marianne  
; APPLICANT: Masucci, James  
; TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL OF GENE EXPRESSION  
; FILE REFERENCE: 38-21(15856)B  
; CURRENT APPLICATION NUMBER: US/09/894,633A  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: 60/214,357  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 09/894,633  
; PRIOR FILING DATE: 2000-06-28  
; NUMBER OF SEQ ID NOS: 111  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 20  
; LENGTH: 28  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(28)  
; OTHER INFORMATION: synthetic primer sequence  
US-09-894-633A-20

Query Match 0.4%; Score 17.4; DB 10; Length 28;  
Best Local Similarity 77.8%; Pred. No. 3.3e+05;  
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db 27 ACAGGGACCGCGCGCTGCTGCTCA 1

RESULT 6  
US-09-791-171-160  
; Sequence 160, Application US/09791171  
; Patent No. US20020094336A1  
; GENERAL INFORMATION:  
; APPLICANT: ANDERSEN, Peter  
; APPLICANT: NIELSEN, Rikke  
; APPLICANT: OETTINGER, Thomas  
; APPLICANT: RASMUSSEN, Peter Birk

; APPLICANT: ROSENKRANDS, Ida  
; APPLICANT: WELDINGH, Karin  
; APPLICANT: FLORIO, Walter  
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS  
; FILE REFERENCE: 670001-2002.1  
; CURRENT APPLICATION NUMBER: US/09/791,171  
; CURRENT FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: 09/050,739  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 0376/97  
; PRIOR FILING DATE: 1997-04-02  
; PRIOR APPLICATION NUMBER: 1277/97  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/044,624  
; PRIOR FILING DATE: 1997-04-18  
; PRIOR APPLICATION NUMBER: 60/070,488  
; PRIOR FILING DATE: 1998-01-05  
; NUMBER OF SEQ ID NOS: 173  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 160  
; LENGTH: 30  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
US-09-791-171-160

Query Match 0.4%; Score 17.4; DB 10; Length 30;  
Best Local Similarity 77.8%; Pred. No. 3.4e+05;  
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3268 TGAGAGCTGGAAACCAAGTGAAC 3294  
||||| || ||| ||||| |||||  
Db 2 TGAGATCTAGATGCCACAGGGAAC 28

RESULT 7  
US-09-804-717A-16  
; Sequence 16, Application US/09804717A  
; Patent No. US20020164311A1  
; GENERAL INFORMATION:  
; APPLICANT: Strom, Terry B.  
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR PREVENTION OF GRAFT REJECTION  
; FILE REFERENCE: 01948-051003  
; CURRENT APPLICATION NUMBER: US/09/804,717A  
; CURRENT FILING DATE: 2002-04-25  
; PRIOR APPLICATION NUMBER: US 09/304,755  
; PRIOR FILING DATE: 1999-05-04  
; PRIOR APPLICATION NUMBER: US 08/273,402  
; PRIOR FILING DATE: 1994-07-11  
; PRIOR APPLICATION NUMBER: US 08/024,569  
; PRIOR FILING DATE: 1993-03-01  
; PRIOR APPLICATION NUMBER: US 07/843,731  
; PRIOR FILING DATE: 1992-02-28  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-804-717A-16

Query Match 0.4%; Score 17.2; DB 9; Length 22;  
Best Local Similarity 86.4%; Pred. No. 3.3e+05;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 878 TTCCGGCAGCGGTGTGTGGACC 899  
||||||| ||||| |||||  
Db 1 TTCCGGCAACAGCTGTGTGGACC 22

RESULT 8  
US-09-866-108-3764

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; Sequence 3764, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 3764
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-3764
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Query Match 0.4%; Score 17; DB 10; Length 25;
Best Local Similarity 80.0%; Pred. No. 3.9e+05;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3367 CTGCGGTCGTGGGACCAAGCACA 3391
Db 1 CTGCGGTCGTGGGACCAAGCACA 25
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RESULT 9
US-09-866-108-3778
; Sequence 3778, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
```

```
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 3778
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-3778
```

```
Query Match 0.4%; Score 17; DB 10; Length 25;
Best Local Similarity 80.0%; Pred. No. 3.9e+05;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2320 GCCCAGACCAAGGAGCTGATGCAC 2344
Db 1 GACCCAGGCCAAGGAGCTGATGCAC 25
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RESULT 10
US-09-866-108-3895/C
; Sequence 3895, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
```



```
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 3895
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-3895
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```
Query Match 0.4%; Score 17; DB 10; Length 25;
Best Local Similarity 80.0%; Pred. No. 3.9e+05;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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```
Qy 727 CTGGGGCGCTGCTACCTCGCGCTC 751
Db 25 CTGGGGCGCTGCTCCTCGCTGTC 1
||| ||||| ||||| ||||| |||
```

```
RESULT 11
US-09-866-108-3945
; Sequence 3945, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
```

```
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 3945
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-3945

Query Match 0.4%; Score 17; DB 10; Length 25;
Best Local Similarity 80.0%; Pred. No. 3.9e+05;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3205 ACTGGGAAACAGAGGAGGAGCA 3229
Db 1 ACCAGGAAAGCAGAGGAGGAGCA 25
||| ||||| ||||| ||||| |||

RESULT 12
US-09-866-108-4394
; Sequence 4394, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
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RESULT 14  
US-09-866-108-12035  
; Sequence 12035, Application US/09866108  
; Patent No. US20020048800A1

```

: GENERAL INFORMATION:
:
: APPLICANT: GU, Yizhong
:
: APPLICANT: JI, Yonggang
:
: APPLICANT: PENN, Sharon G.
:
: APPLICANT: HANZEL, David K.
:
: APPLICANT: RANK, David R.
:
: APPLICANT: CHEN, Wensheng
:
: APPLICANT: SHANNON, Mark
:
: TITLE OF INVENTION: MYOSIN-LIKE GENE EXPR
:
: FILE REFERENCE: AEOmica-7
:
: CURRENT APPLICATION NUMBER: US/09/866,108
:

```

REFERENCE: NAME, DAVEN A.  
 APPLICANT: CHEN, wensheng  
 APPLICANT: SHANNON, Mark  
 TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSION  
 FILE REFERENCE: AEOMICA-7  
 CURRENT APPLICATION NUMBER: US/09/866,108

	Query Match	Score 17:	DB 10:	Length 25:
	Best Local Similarity	80.0%;	Pred. No. 3.9e+05;	
	Matches 20; Conservative	0; Mismatches	5; Indels	
Qy	1792 GAAGCTCGGCATGAAGTCCAGG	1816		
Db	1 GAAGTTGGGAATGAATCCTGGC	25		

```
RESULT 15
US-09-866-108-12894
; Sequence 12894: Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ABOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 12894
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-12894

Query Match 0.4%; Score 17; DB 10; Length 25;
Best Local Similarity 80.0%; Pred. No. 3.9e+05;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Caps 0;

QY 323 AGCACCATCAAGCAGCTGCTGTGGC 347
Db 1 AACACCATCAAGCAGCTGGAGCAGC 25

Search completed: March 4, 2003, 06:46:21
Job time : 1106 secs
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GenCore version 5.1.4\_p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2003, 19:51:57 ; Search time 4726 Seconds  
(without alignments)  
13255.214 Million cell updates/sec

Title: US-10-049-743-1  
Perfect score: 3868  
Sequence: 1 gaattcgacagcgccg.....ggtcttggtacgagaattc 3868

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues 30108  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST.\*  
1: em\_estba.\*  
2: em\_esthum.\*  
3: em\_estin.\*  
4: em\_estmu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_hcc.\*  
9: gb\_estl.\*  
10: gb\_est2.\*  
11: gb\_hcc.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: gb\_gss.\*  
18: em\_gss\_hum.\*  
19: em\_gss\_inv.\*  
20: em\_gss\_pln.\*  
21: em\_gss\_vrt.\*  
22: em\_gss\_fun.\*  
23: em\_gss\_mam.\*  
24: em\_gss\_mus.\*  
25: em\_gss\_other.\*  
26: em\_gss\_pro.\*  
27: em\_gss\_fod.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19.6	0.5	28	14 T47368	T47368 yb13b04.r1
2	18.6	0.5	30	13 BM399411	BM399411 5009-0-57
3	18	0.5	28	9 AL584657	AL584657 AL584657
c 4	17	0.4	29	17 BH861248	BH861248 SALK_0678
c 5	16.8	0.4	26	17 AZ479681	AZ479681 LM0300G02
6	16.8	0.4	26	17 AZ780072	AZ780072 2M0017H04

c	7	16.8	0.4	28	9	AA973948
	8	16.8	0.4	30	13	BM398517
	9	16.6	0.4	27	17	AZ404206
c	10	16.4	0.4	29	17	AZ789420
	11	16.4	0.4	30	17	AZ840149
c	12	16.2	0.4	22	9	AA953755
c	13	16.2	0.4	30	13	BM398127
c	14	16.2	0.4	30	17	AZ343274
c	15	16.2	0.4	30	17	AZ601864
c	16	16	0.4	25	9	AA766400
	17	16	0.4	27	17	TA212C03P
	18	16	0.4	28	17	AZ371129
	19	16	0.4	30	17	AZ343274
	20	16	0.4	30	17	AZ408639
c	21	15.8	0.4	23	17	AZ818371
	22	15.8	0.4	28	9	AA933742
	23	15.8	0.4	28	17	AZ345640
	24	15.8	0.4	28	17	AZ502451
c	25	15.8	0.4	29	9	AU269375
c	26	15.8	0.4	29	14	DA5817
	27	15.8	0.4	30	10	AV852654
c	28	15.8	0.4	30	14	H41620
c	29	15.8	0.4	30	17	BH810436
c	30	15.6	0.4	24	17	AZ308159
c	31	15.6	0.4	24	17	AZ779573
c	32	15.6	0.4	27	13	BM401118
c	33	15.6	0.4	29	17	AZ315608
c	34	15.6	0.4	29	17	AZ476559
c	35	15.4	0.4	26	17	AZ308069
c	36	15.4	0.4	27	17	AZ345323
c	37	15.4	0.4	27	17	AZ404206
c	38	15.4	0.4	28	9	AI006312
c	39	15.4	0.4	29	17	AZ803680
c	40	15.4	0.4	30	17	AZ780802
c	41	15.4	0.4	30	17	AZ822508
c	42	15.2	0.4	20	17	AZ784682
c	43	15.2	0.4	22	17	AZ942905
c	44	15.2	0.4	28	9	AI625245
c	45	15.2	0.4	28	9	AI697335

## ALIGNMENTS

RESULT 1  
T47368  
LOCUS  
DEFINITION  
IMAGE:71023 5' similar to gb:J02683 ADP, ATP CARRIER  
PROTEIN, FIBROBLAST ISOFORM (HUMAN), mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
COMMENT

T47368 28 bp mRNA linear EST 01-FEB-1995  
yb13b04.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone  
IMAGE:71023 5' similar to gb:J02683 ADP, ATP CARRIER  
PROTEIN, FIBROBLAST ISOFORM (HUMAN), mRNA sequence.  
T47368  
T47368.1 GI:649349  
EST.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 28)  
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,  
Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins,  
M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,  
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,  
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,  
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.  
Generation and analysis of 280,000 human expressed sequence tags  
Genome Res. 6 (9), 807-828 (1996)  
Other ESTs: yb13b04.s1  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 89

High quality sequence starts: 1 High quality sequence stops: 1  
Source: IMAGE Consortium, LNL This clone is available royalty-free  
through LNL; contact the IMAGE Consortium (info@image.lnl.gov)  
for further information. Trace considered overall poor quality  
Insert length: 89 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 1.

#### FEATURES

source

1. .28

/organism="Homo sapiens"

/db\_xref="Gene:491920"

/db\_xref="taxon:9606"

/clone\_image="71023"

/clone\_lib="Stratagene placenta (937225)"

/sex="male"

/lab\_host="SOLR cells (kanamycin resistant)"

/note="Organ: placenta; Vector: pBluescript SK-; Site:1:

EcoRI; Site:2: XhoI; Cloned unidirectionally. Primer:

Oligo dT. Caucasian. Average insert size: 1.2 kb; Uni-ZAP

XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGG 3' -3'

adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3'

11 g 6 t

BASE COUNT 4 a 7 c 11 g 6 t

#### ORIGIN

Query Match 0.5%; Score 19.6; DB 14; Length 28;  
Best Local Similarity 84.6%; Pred. No. 3.4e+06;  
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1204 CGAGCGGATGAAGCTGGTGGTGCAGG 1229

||||| | | | | | | | | | | | | | | |

Db 2 CGAGCGGGTCAAGCTGCTGCTGCAGG 27

||||| | | | | | | | | | | | | | | |

RESULT 2

#### BM399411

#### LOCUS

#### DEFINITION

#### ACCESSION

#### VERSION

#### KEYWORDS

#### SOURCE

#### ORGANISM

#### REFERENCE

#### AUTHORS

#### TITLE

#### JOURNAL

#### COMMENT

#### CONTACT

#### UNPUBLISHED

#### CONTACT

#### UNIVERSITY

#### 920 E. 58th Street, Chicago, IL 60637, USA

#### Tel: 773 702 4374

#### Fax: 773 702 3172

#### Email: apturkew@midway.uchicago.edu

#### Seq primer: T3.

#### Location/Qualifiers

#### 1. .30

#### /organism="Tetrahymena thermophila"

#### /strain="CU428.1"

#### /db\_xref="taxon:5911"

#### /clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"

#### /note="Vector: Bluescript2 SK+; Details on library

#### preparation can be found in Chilcoat and Turkewitz (2001)

#### Proc. Natl. Acad. Sci USA, 98: 8709-8713."

#### 4 a 10 c 12 g 4 t

#### BASE COUNT

#### ORIGIN

#### Query Match

#### 0.5%; Score 18.6; DB 13; Length 30;

#### Best Local Similarity

84.0%; Pred. No. 5.9e+06;

Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 719 GCTCAACCTGGGGCTGGTACCC 743

||||| | | | | | | | | | | | | | | |

Db 6 GCTCAGCGTGGGGCCCGGTACCC 30

||||| | | | | | | | | | | | | | | |

RESULT 3

#### AL584657

#### LOCUS

#### DEFINITION

#### ACCESSION

#### VERSION

#### KEYWORDS

#### SOURCE

#### ORGANISM

#### REFERENCE

#### AUTHORS

#### TITLE

#### JOURNAL

#### COMMENT

#### CONTACT

#### UNPUBLISHED

#### CONTACT

#### DEPT. GENOMICS AND BIOINFORMATICS

#### ROSLIN INSTITUTE

#### ROSLIN, MIDLOTHIAN, EH25 9PS, UK

#### Tel: +44 (0)131 527 4200

#### Fax: +44 (0)131 440 0434

#### Email: frazer.murray@bbsrc.ac.uk

#### Seq primer: T3.

#### Location/Qualifiers

#### 1. .28

#### /organism="Gallus gallus"

#### /db\_xref="taxon:9031"

#### /clone="ROS012G12"

#### /clone\_lib="Stratagene Chick Embryo Lambda cDNA Library (\*

#### 937405)"

#### /tissue\_type="Embryo"

#### /dev\_stage="5 days old"

#### /lab\_host="SOLR cells (kanamycin resistant)"

#### /note="Vector: pBLUESCRIPT SK; Site:1: EcoRI; Site:2: XhoI

#### ; Cloned unidirectionally. Primer: Oligo dT. Uni-ZAP XR

#### vector. Average insert size: 1.5kb.; 5' adaptor sequence:

#### 5' GAATTCGGCAGG 3'; 3' adaptor sequence: 5'

#### CTCGAGTTTTTTTTTTT 3'"

#### 8 a 7 c 11 g 2 t

#### BASE COUNT

#### ORIGIN

#### Query Match

0.5%; Score 18; DB 9; Length 28;

Best Local Similarity 100.0%; Pred. No. 7.8e+06;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCGGCAGCAGCGGC 18

||||| | | | | | | | | | | | | | | |

Db 1 GAATTCGGCAGCAGCGGC 18

||||| | | | | | | | | | | | | | | |

RESULT 4

#### BH861248/c

#### LOCUS

#### DEFINITION

#### ACCESSION

#### VERSION

#### KEYWORDS

#### SOURCE

#### ORGANISM

#### REFERENCE

#### AUTHORS

#### TITLE

#### JOURNAL

#### COMMENT

#### CONTACT

#### UNPUBLISHED

#### CONTACT

#### DEPT. GENOMICS AND BIOINFORMATICS

#### ROSLIN INSTITUTE

#### ROSLIN, MIDLOTHIAN, EH25 9PS, UK

#### Tel: +44 (0)131 527 4200

#### Fax: +44 (0)131 440 0434

#### Email: frazer.murray@bbsrc.ac.uk

#### Seq primer: T3.

#### Location/Qualifiers

#### 1. .28

#### /organism="Gallus gallus"

#### /db\_xref="taxon:9031"

#### /clone="ROS012G12"

#### /clone\_lib="Stratagene Chick Embryo Lambda cDNA Library (\*

#### 937405)"

#### /tissue\_type="Embryo"

#### /dev\_stage="5 days old"

#### /lab\_host="SOLR cells (kanamycin resistant)"

#### /note="Vector: pBLUESCRIPT SK; Site:1: EcoRI; Site:2: XhoI

#### ; Cloned unidirectionally. Primer: Oligo dT. Uni-ZAP XR

#### vector. Average insert size: 1.5kb.; 5' adaptor sequence:

#### 5' GAATTCGGCAGG 3'; 3' adaptor sequence: 5'

#### CTCGAGTTTTTTTTTTT 3'"

#### 8 a 7 c 11 g 2 t

#### BASE COUNT

#### ORIGIN

#### Query Match

0.5%; Score 18; DB 9; Length 28;

Best Local Similarity 100.0%; Pred. No. 7.8e+06;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCGGCAGCAGCGGC 18

||||| | | | | | | | | | | | | | | |

Db 1 GAATTCGGCAGCAGCGGC 18

||||| | | | | | | | | | | | | | | |

RESULT 4

#### BH861248/c

#### LOCUS

#### DEFINITION

#### ACCESSION

#### VERSION

#### KEYWORDS

#### SOURCE

#### ORGANISM

#### REFERENCE

#### AUTHORS

#### TITLE

#### JOURNAL

#### COMMENT

#### CONTACT

#### UNPUBLISHED

#### CONTACT

#### DEPT. GENOMICS AND BIOINFORMATICS

#### ROSLIN INSTITUTE

#### ROSLIN, MIDLOTHIAN, EH25 9PS, UK

#### Tel: +44 (0)131 527 4200

#### Fax: +44 (0)131 440 0434

#### Email: frazer.murray@bbsrc.ac.uk

#### Seq primer: T3.

#### Location/Qualifiers

#### 1. .28

#### /organism="Gallus gallus"

#### /db\_xref="taxon:9031"

#### /clone="ROS012G12"

#### /clone\_lib="Stratagene Chick Embryo Lambda cDNA Library (\*

#### 937405)"

#### /tissue\_type="Embryo"

#### /dev\_stage="5 days old"

#### /lab\_host="SOLR cells (kanamycin resistant)"

#### /note="Vector: pBLUESCRIPT SK; Site:1: EcoRI; Site:2: XhoI

#### ; Cloned unidirectionally. Primer: Oligo dT. Uni-ZAP XR

#### vector. Average insert size: 1.5kb.; 5' adaptor sequence:

#### 5' GAATTCGGCAGG 3'; 3' adaptor sequence: 5'

#### CTCGAGTTTTTTTTTTT 3'"

#### 8 a 7 c 11 g 2 t

#### BASE COUNT

#### ORIGIN

#### Query Match

0.5%; Score 18; DB 9; Length 28;

Best Local Similarity 100.0%; Pred. No. 7.8e+06;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCGGCAGCAGCGGC 18

||||| | | | | | | | | | | | | | | |

Db 1 GAATTCGGCAGCAGCGGC 18

||||| | | | | | | | | | | | | | | |

RESULT 4

#### BH861248/c

#### LOCUS

#### DEFINITION

#### ACCESSION

#### VERSION

#### KEYWORDS

#### SOURCE

#### ORGANISM

#### REFERENCE

#### AUTHORS

#### TITLE

#### JOURNAL

#### COMMENT

#### CONTACT

#### UNPUBLISHED

#### CONTACT

#### DEPT. GENOMICS AND BIOINFORMATICS

#### ROSLIN INSTITUTE

#### ROSLIN, MIDLOTHIAN, EH25 9PS, UK

#### Tel: +44 (0)131 527 4200

#### Fax: +44 (0)131 440 0434

#### Email: frazer.murray@bbsrc.ac.uk

#### Seq primer: T3.

#### Location/Qualifiers

1 (bases 1 to 29)  
Alonso,J.M., Lelise,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab  
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.  
, Zimmerman,J. and Ecker,J.R.  
A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
Unpublished (2001)  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: eckers@salk.edu  
This is single pass sequence recovered from the left border of  
DNA. This sequence lies within an annotated intron of At5g40020.  
Class: TDNA tagged.

FEATURES  
source  
1. .29  
Location/Qualifiers  
/organism="Arabidopsis thaliana"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone\_lib="SALK\_067873"  
/clone="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

BASE COUNT 12 a 3 c 5 g 9 t  
ORIGIN

Query Match 0.4%; Score 17; DB 17; Length 29;  
Best Local Similarity 80.0%; Pred. No. 1.3e+07;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3464 CACTGGTATTATTTATGACTTTGA 3488  
||||| ||||| ||||| ||||| |||||  
Db 25 CAATGTTAATATCTTTATGACTTTGA 1

RESULT 5  
AZ479681/c  
LOCUS  
DEFINITION  
1M0300G02R Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
clone UUGCLM0300G02 R, DNA sequence.  
ACCESSION  
AZ479681  
VERSION  
AZ479681.1 GI:10639845  
KEYWORDS  
GSS.  
SOURCE  
house mouse.  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 26)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0300 row: G column: 02  
Seq primer: CACACAGAAACAGCTATGACC

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Class: plasmid ends  
High quality sequence stop: 26.  
Location/Qualifiers  
1. .26  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGCLM0300G02"  
/clone\_lib="Mouse 10kb plasmid UUGCLM library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gii4732114|gbiAF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 13 a 0 c 13 g 0 t  
ORIGIN

Query Match 0.4%; Score 16.8; DB 17; Length 26;  
Best Local Similarity 90.0%; Pred. No. 1.4e+07;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3110 CTTCTCTCTCTCACCTCTT 3129  
||||| ||||| ||||| |||||  
Db 26 CTTCTCTCTCTCTCTCTT 7

RESULT 6  
AZ780072  
LOCUS  
DEFINITION  
2M017H04F Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
clone UUGCLM0017H04 F, DNA sequence.  
ACCESSION  
AZ780072  
VERSION  
AZ780072.1 GI:12911368  
KEYWORDS  
GSS.  
SOURCE  
house mouse.  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 26)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0017 row: H column: 04  
Seq primer: CGTTGTAAACACGCGCCAGT

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

```

Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
1. .26
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGG2M0017H04"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      8 a      6 c      6 g      6 t
ORIGIN
Query Match      0.4%; Score 16.8; DB 17; Length 26;
Best Local Similarity 90.0%; Pred. No. 1.4e+07;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2851 CACATATGCTGGGGCATTG 2870
||||||| ||||| |||||
Db 1 CACATATGCTGGGGCATTG 20

RESULT 7
AA973948/c      28 bp mRNA linear EST 23-JUL-1998
LOCUS
DEFINITION
Og12d02.s1 NCI_CGAP_GC4 Homo sapiens CDNA clone IMAGE:1586115 3'
similar to TR:Q35787 Q35787 KINESIN-RELATED PROTEIN. ;, mRNA
sequence.
ACCESSION      AA973948.1 GI:3149128
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 28)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapb-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert length: 790 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. .28
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1586115"
/clone_lib="NCI_CGAP_GC4"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."
BASE COUNT      6 a      3 c      11 g      8 t
ORIGIN
Query Match      0.4%; Score 16.8; DB 9; Length 28;
Best Local Similarity 75.0%; Pred. No. 1.5e+07;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3164 AGCTGCTCAAGACATCCAGTATCTCA 3191
||||| ||||| ||||| |||||
Db 28 ACCTCTACATTCACATCCAGGACCTCA 1

RESULT 8
BM398517
LOCUS
DEFINITION
5009-0-46-D07.t.1 Chilcoat/Turkewitz CDNA (large fraction)
Tetrahymena thermophila CDNA, mRNA sequence.
ACCESSION      BM398517.1 GI:18198570
VERSION
KEYWORDS
SOURCE
ORGANISM
Tetrahymena thermophila.
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 30)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel
,J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1. .30
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz CDNA (large fraction)"
/notes="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT      4 a      10 c      13 g      3 t
ORIGIN
Query Match      0.4%; Score 16.8; DB 13; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.5e+07;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 715 CTCGGCTCAAACCTGGGGCGCTGGTACC 742
||||| ||||| ||||| |||||

```



```

Db      3  CTGAGCTCAGCGGGGGGCGCGGTACC 30

RESULT 9
AZ404206
LOCUS   LM0172120F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION
clone UUGC1M0172120 F, DNA sequence.
ACCESSION
AZ404206
VERSION
AZ404206.1 GI:10528219
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1 (bases 1 to 27)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0172 row: I column: 20
Seq primer: CTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 27.
FEATURES
Location/Qualifiers
1..27
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0172120"
/clone.lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT
0 a 9 c 9 g 9 t
ORIGIN
Query Match 0.4%; Score 16.6; DB 17; Length 27;
Best Local Similarity 82.6%; Pred. No. 1.6e+07;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 2030 CTCTGCAGCTCGTGCAGTGTCT 2052
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Db      1  CTGCTGCTGCTGCTGCTGCTGCT 23

RESULT 10
AZ789420/c
LOCUS   2M0037J11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION
clone UUGC2M0037J11 F, DNA sequence.
ACCESSION
AZ789420
VERSION
AZ789420.1 GI:12930223
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1 (bases 1 to 29)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0037 row: J column: 11
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 29.
FEATURES
Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0037J11"
/clone.lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT
8 a 7 c 6 g 8 t
ORIGIN
Query Match 0.4%; Score 16.4; DB 17; Length 29;
Best Local Similarity 76.9%; Pred. No. 1.8e+07;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 3249 AGTTTACGAGCGCTCCGTGAGAGC 3274
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```





/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
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polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gil4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT           8 a           3 c           11 g           8 t  
ORIGIN

Query Match           0.4%;   Score 16.2;   DB 17;   Length 30;  
Best Local Similarity   72.4%;   Pred. No. 2e+07;  
Matches   21;   Conservative   0;   Mismatches   8;   Indels   0;   Gaps   0;  
  
Qy   2983   TGTCCCATTCATCCTCACCCTACGACTTTG 3011  
          |||||||   |||||   |   |||   ||  
Db   29   TGTCCCATGCATCCTATCAACACCACCATG 1

Search completed: March 4, 2003, 06:25:19  
Job time : 4732 secs